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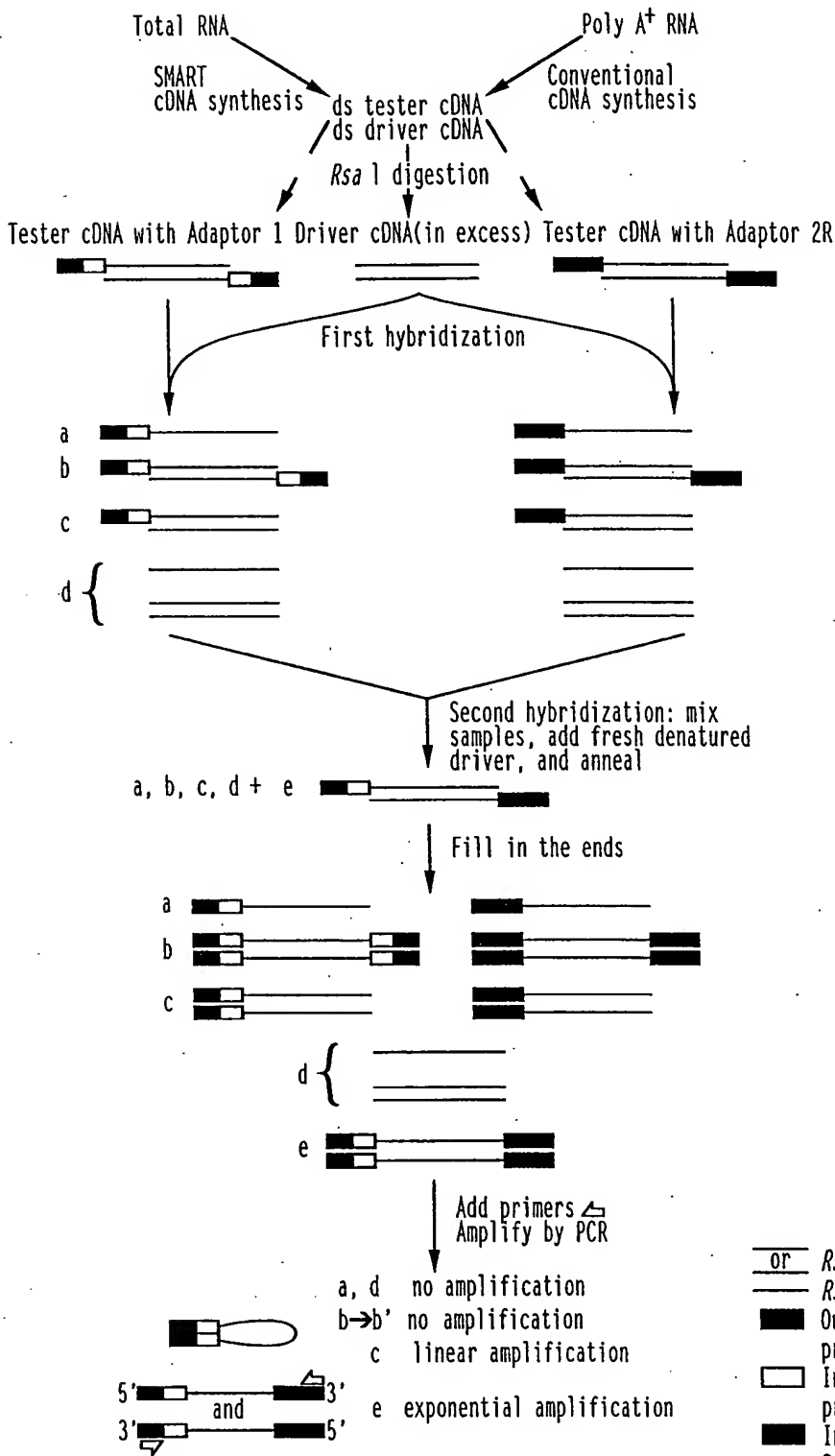
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**FIG. 1**



Prepare cDNA by either SMART or conventional synthesis.

Separately digest tester and driver ds cDNA to obtain shorter, blunt-ended fragments.

Divide tester cDNA into 2 portions and ligate each portion to a different adaptor. Driver cDNA has no adaptors.

Hybridization kinetics lead to equalization and enrichment of differentially expressed sequences among ss tester molecules.

Generate templates for PCR amplification from differentially expressed sequences.

Due to suppression PCR, only differentially expressed sequences are amplified exponentially.

mICACC-1 cDNA Translated Sequence  
Sequence Range: 1 to 2931

FIG. 2A

```

1                                     ctgcagg

8  atggaatctttgaagagtcctgtcttcctcttgatcctccacctt
   M E S L K S P V F L L I L H L
53 ctggaaggagttctgagtgagtcctcatccaactgaacaacaac
   L E G V L S E S L I Q L N N N
98 ggctatgagggcatcgatcgccatagaccacgacgtgccggaa
   G Y E G I V I A I D H D V P E
143 gatgaagccctcattcaacacataaaggacatggtgactcaggcc
   D E A L I Q H I K D M V T Q A
188 tctccatacctgtttgaagctacaggaaaaagattttacttcaaa
   S P Y L F E A T G K R F Y F K
233 aatgttgccattttgattcccagagagctggaaggcaaagcctgaa
   N V A I L I P E S W K A K P E
278 tatacagggccaaaacttgaaaccttcaaaaacgctgatgtcctt
   Y T R P K L E T F K N A D V L
323 gtatcaacaaccagccctctaggcaatgatgagccctacaccgaa
   V S T T S P L G N D E P Y T E
368 catataggagcatgtggagaaaaaggggatcaggattcacctgact
   H I G A C G E K G I R I H L T
413 cctgacttcttagcaggaaagaagctgactcagtatgggccacaa
   P D L A G K K L T Q Y G P Q
458 gacaggacctttgtccatgagtgggctcacttccgatggggagtg
   D R T F V H E W A H F R W G V
503 tttaatgaatacaacaacgacgagaagttctacttatccaaagga
   F N E Y N N D E K F Y L S K G
548 aaacccaagcagtgaggtgttcagcagccattaccggtaaaaaat
   K P Q A V R C S A A I T G K N
593 caagttcgtcgtgccaggaggagcagttgtatcactaacggaaaag
   Q V R R C Q G G S C I T N G K
638 tgtgtaatcgacagagtaacgggactgtataaagacaattgtgta
   C V I D R V T G L Y K D N C V
683 tttgtaccagatccacacccaaaacgagaaggcttccatcatgttt
   F V P D P H Q N E K A S I M F
728 aacccaaatatcaattctgtggttgaattctgtacagaaaaaaat
   N Q N I N S V V E F C T E K N
773 cacaatcaagaagccccaatgacccaaaaccaacgatgcaatctc
   H N Q E A P N D Q N Q R C N L
818 cgaagcacgtgggaagtcacccaggaatctgaggacttcaagcaa
   R S T W E V I Q E S E D F K Q
863 accactcccatgacagcccagccacctgcacccaccttctcactg
   T T P M T A Q P P A P T F S L
908 ctgcaaattggacaaaagaattgtgtgcttagttcttgataagtcc
   L Q I G Q R I V C L V L D K S
953 gggagcatgctgaacgatgatcgctttaaccgaatgaatcaggca
   G S M L N D D R L N R M N Q A
998 agccggcttttctgctgcagactgtggagcagggatcctgggtc
   S R L F L L Q T V E Q G S W V

```



FIG. 2C

2168 caagacaagcagctgtgcttcagcaggacatcttcagggggatcg  
Q D K Q L C F S R T S S G G S  
2213 tttgtggccaccaatgtccccgcagcagctcccatcctgacctc  
F V A T N V P A A A P I P D L  
2258 tttccaccctgtcaaatactgacctgaaggccagcatccaaggg  
F P P C Q I T D L K A S I Q G  
2303 cagaacctggtgaatctgacgtggacggctcctggggatgactac  
Q N L V N L T W T A P G D D Y  
2348 gaccacgggagagcttccaactacatcatccgaatgagcaccagt  
D H G R A S N Y I I R M S T S  
2393 atcggtgatctcagggaccacttcaacacctcactccaagtgaac  
I V D L R D H F N T S L Q V N  
2438 actaccggtcttatccccaaagaggccagctctgaggaaatcttt  
T T G L I P K E A S S E E I F  
2483 gagtttgaactgggaggcaacacttttggaaatggcacagatatc  
E F E L G G N T F G N G T D I  
2528 ttcattgctatccaggctgtggataagtccaatctgaaatcagaa  
F I A I Q A V D K S N L K S E  
2573 atctccaacattgcacgggtgtctgtgttcatccccgctcaggag  
I S N I A R V S V F I P A Q E  
2618 ccgccccattccccgaagactcaactcccccttgtcctgacatcagc  
P P I P E D S T P P C P D I S  
2663 atcaacagcaccattcctggcatccacgtgctgaagataatgtgg  
I N S T I P G I H V L K I M W  
2708 aagtggttaggggaaatgcagggtgacactagggtttgcactga  
K W L G E M Q V T L G L H \*  
  
2750 attttcaggcaagaaatcaaccagtcattcctttcactgggagaat  
  
2795 tttctaaaaatgtacttttagacttctgtagggggcggtatagta  
  
2840 acactcgaagctgtaaaaactgggtctgggtgcattaaaaattatc  
  
2885 tgttcaaatacaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa  
  
2930 aa

## FIG. 3A

CLUSTAL W (1.82) sequence alignment of mICACC-1 and bovine CACC (b-CACC)

```

mICACC-1: MESLKSPVFLILHLLEGVLSESLIQLNNNGYEGIVIAIDHDVPEDEALIQHIKDMVTQA 60
b-CACC:   MVPRLTVILFLTLHLLPG-MKSSMVNLINNGYDGIVIAINPSVPEDEKLIQNIKEMVTEA 59

mICACC-1: SPYLFEATGKRIFYFKNVAILIPESWKAKPEYTRPKLETFTKNADVLVSTTSPLGNDEPYTE 120
b-CACC:   STYLFHATKRRVYFRNVSILIPMTWKSSEYLMKQESYDQAEVIVANPYLKHGDDPYTL 119

mICACC-1: HIGACGEKGIRIHLTPDFLAGKKLTQYGPQDRFTVHEWAHFRWGVFNEYNNDEKFYLSK- 179
b-CACC:   QYGRCGEKGQYIHFTPNFLLTNNLPIYGSRGRAFVHEWAHLRWGIFDEYNGDQPFYISRR 179

mICACC-1: GKPQAVRCSAAITGKNQVRRRCQGGSCITNGKCVIDRVTGLYKDNCVFVDPDPHQNEKASIM 239
b-CACC:   NTIEATRCSTHITGTNVIVKCQGGSCITR-PCRRDSQTGLYEAKCTFIPEKSQTARES IM 238

mICACC-1: FNQNINSVVEFCTEKNHNQEAPNDQNQRCLNRSTWEVIEQSEDFKQTTPTMTAQQP--APT 297
b-CACC:   FMQSLHSVTEFCTEKTHNVEAPNLQNKMCNGKSTWDVIMNSTDFQNTSPMTEMNPPTQPT 298

mICACC-1: FSL LQIGQRIVCLVLDKSGSMLNDDRLNRMNQASRLFLLQTVEQGSWVGMVTFDSAAYVQ 357
b-CACC:   FSL LKSKQRVVCLVLDKSGSMSEDRLFRMNQAAELFLIQIIEKGS LVGMVTFDSVAEIR 358

mICACC-1: SELKQLNSGADRDLLIKHLPTVSAGGTSICSGLRTAFT-VIKKKYPTDGSEIVLLTDGED 416
b-CACC:   NNLTKITDDNVYENITANLPQEANGGTSICRGLKAGFQAI IQSQQSTSGSEIILLTDGED 418

mICACC-1: NTISSCFDLVKQSGAIIHTVALGPAAAKELEQLSKMTGGLQTYSSDQVQNNGLVDAFAAL 476
b-CACC:   NEIHSCIEEVKQSGV I IHTIALGPSAAKELETLSDMTGGRFYANKDIN--GLTNAFSRI 476

mICACC-1: SSGNAAIAQHSIQLESRGVNLQNNQWMNGSVIVDSSVGKDTLFLITWTTHPPTIFIWDPS 536
b-CACC:   SSRSGSITQQTIQLESKALAITKKWVNGTVPVDSTIGNDTFFVVTWTIKKPEILLQDPK 536

mICACC-1: G--VEQNGFILD TT-TKVAYLQVPGTAKVGFWKYSIQ--ASSQTLTLTVTSRAASATLP 590
b-CACC:   GKKYKTSDFKEDKLN IHSARLRIPGIAETGTWYSLNNHAS PQILTVTVTTRARSPTTP 596

mICACC-1: PITVTPVVNKNTGKFPSPVTYASIRQGASPI LRASVTALIESVNGKTVTLELLDNGAGA 650
b-CACC:   PVTATAHMSQNTAHYPSPIVIVYAQVSQGFLPVLGINVTAI IETEDGHQVTLELWDNGAGA 656

mICACC-1: DATKNDGVYSRFFTA FDANGRYSVKI WALGGVTS DRQRAAPPKNRMYIDGWIEDGEVRM 710
b-CACC:   DTVKNDGIYSRYFTDYRGNGRYS LKVHAEARNNTARLSLRQPQN KALYIPGYIENGKIIL 716

mICACC-1: NPPRPETS--YVQDKQLCFSRTSSGGSFVATNVPA AAPIPDLFPPCQITDLKASIQQQNL 768
b-CACC:   NPPRPEVKDDLAKAEIEDFSRLTSGGSFTVSGAPPGN-HPSVLPPNKI IDLEAKFK-EDH 774

```

## FIG. 3B

mICACC-1: VNLTWTAPGDDYDHGRASNYIIRMSTSIVDLRDHFNTSLQVNTTGLIPKEASSEEIFEFE 828  
b-CACC: IQLSWTAPANVLDKGKANSYIIRISKSFLDLQKDFDNATLVNTSSLKPKEAGSDENFEFK 834

mICACC-1: LGGNTFGNGTDIFIAIQAVDKSNLKSEISNIARVSVFIPAQEPPPIPEDSTPPCPDISINS 888  
b-CACC: PEPFRIENGNTNFYIAVQAINNEANLTSEVSNIAQAIFIP-----MPEDSVP-ALGTKISA 888

mICACC-1: TIPGIHVLKIMWKWLGEQVTLGLH 913  
b-CACC: INLAIFALAMILSIV----- 903

hICACC-2 Translated Sequence  
Sequence Range: 1 to 3190

FIG. 4A1

```
1          cttcttgtgttctttaacccttgcaagtt
30 cagraagaaacccatctgcatccatattgaaaacctgacacaatg
75 tatgcagcaggctcagtgtagtggaactggaggcttctctacaac
120 atgacccaaaggagcattgcaggctcctatTTGCAACCTGAAGTTT
    M T Q R S I A G P I C N L K F
165 gtgactctcctggttgcttaagttcagaactcccattcctggga
    V T L L V A L S S E L P F L G
210 gctggagtacagcttcaagacaatgggtataatggattgctcatt
    A G V Q L Q D N G Y N G L L I
255 gcaattaatcctcaggtacctgagaatcagaacctcatctcaaac
    A I N P Q V P E N Q N L I S N
300 attaagaaatgataactgaagcttcattttacctattttaatgct
    I K E M I T E A S F Y L F N A
345 accaagagaagagtatTTTTcagaaatataaagattttaataacct
    T K R R V F F R N I K I L I P
390 gccacatggaaagctaataataacagcaaaaataaaacaagaatca
    A T W K A N N N S K I K Q E S
435 tatgaaaaggcaaatgtcatagtgactgactggtatagggcacat
    Y E K A N V I V T D W Y R A H
480 ggagatgatccatacacccctacaatacacagagggtgtggaaaagag
    G D D P Y T L Q Y R G C G K E
525 ggaaaatacattcatttcacacctaatttcctactgaatgataac
    G K Y I H F T P N F L L N D N
570 ttaacagctggctacggatcacgaggccgagtgtttgtccatgaa
    L T A G Y G S R G R V F V H E
615 tgggcccacctccgttgggggtgtgttcgatgagtataacaatgac
    W A H L R W G V F D E Y N N D
660 aaacctttctacataaatgggcaaaatcaaattaaagtgacaagg
    K P F Y I N G Q N Q I K V T R
705 tgttcacatgacatcacaggcatttttgtgtgtgaaaaaggctcct
    C S S D I T G I F V C E K G P
750 tgcccccaagaaaactgtattattagtaagctttttaagaagga
    C P Q E N C I I S K L F K E G
795 tgcacctttatctacaatagcacccaaagtgcaactgcatcaata
    C T F I Y N S T Q S A T A S I
840 atgttcatgCGAAGTTTatcttctgtgggtgaattttgtaatgca
    M F M R S L S S V V E F C N A
885 agtaccacacaaccaagaagcaccaaacctacagaaccagatgtgc
    S T H N Q E A P N L Q N Q M C
930 agcctcagaagtgcattgggatgtaatcacagactctgctgacttt
    S L R S A W D V I T D S A D F
975 caccacagctttcccatgaacgggactgagcttccacctcctccc
    H H S F P M N G T E L P P P P
1020 acattctcgctttagaggctgggtgacaaagtggctctgtttagtg
    T F S L V E A G D K V V C L V
```

FIG. 4A2

1065 ctggatgcgtccagcaagatggcagaggctgacagactccttcaa  
L D A S S K M A E A D R L L Q  
1110 ctacaacaagccgcagaattttatgtgatgcagattgttgaaatt  
L Q Q A A E F Y L M Q I V E I  
1155 cataccttcgtgggcattggccagtttcgacagcaaaggagagatc  
H T F V G I A S F D S K G E I  
1200 agagcccagctacaccaaattaacagcaatgatgatcgaaagttg  
R A Q L H Q I N S N D D R K L  
1245 ctgggtttcatactctgcccaccactgtatcagctaaaacagacatc  
L V S Y L P T T V S A K T D I  
1290 agcatttgttcagggcttaagaaaggatttgagggtggttgaaaaa  
S I C S G L K K G F E V V E K  
1335 ctgaatggaaaagcttatggctctgtgatgatattagtgaccagc  
L N G K A Y G S V M I L V T S  
1380 ggagatgataagcttcttggcaattgcttaccactgtgctcagc  
G D D K L L G N C L P T V L S  
1425 agtggttcaacaattcactccattggcctgggttcattctgcagcc  
S G S T I H S I A L G S S A A  
1470 ccaaactctggaggaattatcacgtcttacaggaggtttaaagtcc  
P N L E E L S R L T G G L K F  
1515 tttgttccagatatatcaaactccaatagcatgattgatgctttc  
F V P D I S N S N S M I D A F  
1560 agtagaatttccctctggaactggagacattttccagcaacatatt  
S R I S S G T G D I F Q Q H I  
1605 cagcttgaaagtacaggtgaaaatgtcaaacctcaccatcaattg  
Q L E S T G E N V K P H H Q L  
1650 aaaaacacagtgactgtggataatactgtgggcaacgacactatg  
K N T V T V D N T V G N D T M  
1695 tttctagttacgtggcaggccagtggtcctcctgagattatatta  
F L V T W Q A S G P P E I I L  
1740 tttgatcctgatggacgaaaatactacacaaataattttatcacc  
F D P D G R K Y Y T N N F I T  
1785 aatctaacttttcggacagctagtctttggattccaggaacagct  
N L T F R T A S L W I P G T A  
1830 aagcctgggcactggacttacaccctgaacaatacccatcattct  
K P G H W T Y T L N N T H H S  
1875 ctgcaagccctgaaagtgacagtgaacctctcgtgcctccaactca  
L Q A L K V T V T S R A S N S  
1920 gctgtgccccagccactgtggaagcctttgtggaaagagacagc  
A V P P A T V E A F V E R D S  
1965 ctccattttcctcatcctgtgatgatttatgccaatgtgaaacag  
L H F P H P V M I Y A N V K Q  
2010 ggatttttatcccattcttaatgccactgtcactgccacagttgag  
G F Y P I L N A T V T A T V E  
2055 ccagagactggagatcctgttacgctgagactccttgatgatgga  
P E T G D P V T L R L L D D G  
2100 gcaggtgctgatgttataaaaaatgatggaatttactcgaggtat  
A G A D V I K N D G I Y S R Y  
2145 tttttctcctttgctgcaaatggtagatatagcttgaaagtgcac  
F F S F A A N G R Y S L K V H

FIG. 4A3

2190 gtcaatcactctcccagcataagcacccccagcccactctattcca  
V N H S P S I S T P A H S I P  
2235 gggagtcattgctatgtatgtaccagggttacacagcaaacggtaat  
G S H A M Y V P G Y T A N G N  
2280 attcagatgaatgctccaaggaaatcagtaggcagaaatgaggag  
I Q M N A P R K S V G R N E E  
2325 gagcgaaaagtggggcttttagccgagtcagctcaggaggctccttt  
E R K W G F S R V S S G G S F  
2370 tcagtgtctgggagttccagctggccccaccctgatgtgtttcca  
S V L G V P A G P H P D V F P  
2415 ccatgcaaaattattgacctggaagctgtaaaagttagaaggaa  
P C K I I D L E A V K V E E E  
2460 ttgaccctatcttggacagcacctggagaagactttgatcagggc  
L T L S W T A P G E D F D Q G  
2505 caggctacaagctatgaaataagaatgagtaaaagtctacagaat  
Q A T S Y E I R M S K S L Q N  
2550 atccaagatgactttaacaatgctatttttagtaaatacatcaaag  
I Q D D F N N A I L V N T S K  
2595 cgaaatcctcagcaagctggcatcagggagatatttacgttctca  
R N P Q Q A G I R E I F T F S  
2640 cccagatttccacgaatggacctgaacatcagccaaatggagaa  
P Q I S T N G P E H Q P N G E  
2685 acacatgaaagccacagaatttatgttgcaatacagagcaatggat  
T H E S H R I Y V A I R A M D  
2730 aggaactccttacagtctgctgtatctaacattgcccaggcgct  
R N S L Q S A V S N I A Q A P  
2775 ctgtttattccccccaattctgatcctgtacctgccagagattat  
L F I P P N S D P V P A R D Y  
2820 cttatattgaaaggagttttaacagcaatgggtttgataggaatc  
L I L K G V L T A M G L I G I  
2865 atttgccttattatagttgtgacacatcatactttaagcaggaaa  
I C L I I V V T H H T L S R K  
2910 aagagagcagacaagaaagagaatggaacaaaattattataa  
K R A D K K E N G T K L L \*  
  
2952 ataaatatccaaagtgtcttccttcttagatataagacccatggc  
  
2997 cttcgactacaaaaacataactaaciaaagtcaaattaacatcaaaa  
  
3042 ctgtattaaaaatgcattgagttttgtacaatacagataagatttt  
  
3087 tacatggtagatcaacaaattctttttgggggtagattagaaaac  
  
3132 cttacacttttggctatgaacaaataataaaaaattattctttaaaa  
  
3177 aaaaaaaaaaaaaa 3190

**FIG. 4B1**

hICACC-1

Sequence Range: 1 to 2745

```
1 atggggccattttaagagttctgtgttcaccttgattcttcacctt
  M G P F K S S V F T L I L H L
46 ctagaaggggcccctgagtaattcattcagctgaacaacaat
  L E G A L S N S L I Q L N N N
91 ggctatgaaggcattgtcgttgcaatcgacccaatgtgccagaa
  G Y E G I V V A I D P N V P E
136 gatgaaacactcattcaacaaataaaggacatggtgacccaggca
  D E T L I Q Q I K D M V T Q A
181 tctctgtatctgtttgaagctacaggaaagcgattttattttcaaa
  S L Y L F E A T G K R F Y F K
226 aatgttgccattttgattcctgaaacatggaagacaaaggctgac
  N V A I L I P E T W K T K A D
271 tatgtgagacaaaacttgagacctacaaaaatgctgatgttctg
  Y V R P K L E T Y K N A D V L
316 gttgctgagtctactcctccaggtaatgatgaaccctacactgag
  V A E S T P P G N D E P Y T E
361 cagatgggcaactgtggagagaagggtgaaaggatccacctcact
  Q M G N C G E K G E R I H L T
406 cctgatttcattgcaggaaaaaagttagctgaatatggaccacaa
  P D F I A G K K L A E Y G P Q
451 ggtagggcattttgtccatgagtgggctcatctacgatggggagta
  G R A F V H E W A H L R W G V
496 tttgacgagtacaataatgatgagaaattctacttatccaatgga
  F D E Y N N D E K F Y L S N G
541 agaatacaagcagtaagatgttcagcagggtattactggtacaaat
  R I Q A V R C S A G I T G T N
586 gtagtaaaagaagtgtcagggaggcagctgttacaccaaaaagatgc
  V V K K C Q G G S C Y T K R C
631 acattcaataaagtwacaggactctatgaaaaaggatgtgagttt
  T F N K V T G L Y E K G C E F
676 gttctccaatcccgccagacggagaaggcttctataatgtttgca
  V L Q S R Q T E K A S I M F A
721 caacatgttgattctatagttgaattctgtacagaacaaaaccac
  Q H V D S I V E F C T E Q N H
766 aacaaagaagctccaaacaagcaaaaatcaaaaatgcaatctccga
  N K E A P N K Q N Q K C N L R
811 agcacatgggaagtgatccgtgattctgaggactttaagaaaacc
  S T W E V I R D S E D F K K T
856 actcctatgacaacacagccaccaaatacccaccttctcattgctg
  T P M T T Q P P N P T F S L L
901 cagattggacaaaagaattgtgtgttttagtccttgacaaatctgga
  Q I G Q R I V C L V L D K S G
946 agcatggcgactggtaaccgcctcaatcgactgaatcaagcaggc
  S M A T G N R L N R L N Q A G
991 cagcttttctgctgcagacagttgagctgggggtcctggggtggg
  Q L F L L Q T V E L G S W V G
1036 atgggtgacatttgacagtgctgcccattgtacaaagtgaactcata
  M V T F D S A A H V Q S E L I
1081 cagataaacagtggtcagtgacagggaacacactcgccaaaagatta
  Q I N S G S D R D T L A K R L
1126 cctgcagcagcttcaggaggacgtccatctgcagcgggcttcga
  P A A A S G G T S I C S G L R
```

## FIG. 4B2

```

1171 tcggcatttactgtgattaggaagaaatatccaactgatggatct
    S A F T V I R K K Y P T D G S
1216 gaaattgtgctgctgacggatggggaagacaacactataagtggg
    E I V L L T D G E D N T I S G
1261 tgctttaacgaggtcaaacaaagtggcgccatcatccacacagtc
    C F N E V K Q S G A I I H T V
1306 gcttttggggccctctgcagctcaagaactagaggagctgtccaaa
    A L G P S A A Q E L E E L S K
1351 atgacaggaggtttacagacatatgcttcagatcaagttcagaac
    M T G G L Q T Y A S D Q V Q N
1396 aatggcctcattgatgcttttggggccctttcatcaggaaatgga
    N G L I D A F G A L S S G N G
1441 gctgtctctcagcgctccatccagcttgagagtaagggattaacc
    A V S Q R S I Q L E S K G L T
1486 ctccagaacagccagtggatgaatggcacagtgatcgaggacagc
    L Q N S Q W M N G T V I V D S
1531 accgtgggaaaggacactttgtttcttatcacctggacaacgcag
    T V G K D T L F L I T W T T Q
1576 cctcccaaataccttctctgggatcccgatggacagaagcaagg
    P P Q I L L W D P S G Q K Q G
1621 ggctttgtagtggacaaaaacaccaaataatggcctacctccaaatc
    G F V V D K N T K M A Y L Q I
1666 ccaggcattgctaagggtggcacttggaaatacagtcctgcaagca
    P G I A K V G T W K Y S L Q A
1711 agctcacaaaccttgaccctgactgtcacgtcccgtgcgtccaat
    S S Q T L T L T V T S R A S N
1756 gctacctgacctccaattacagtgacttccaaaacgaacaaggac
    A T L P P I T V T S K T N K D
1801 accagcaaattccccagccctctggtagtttatgcaaatattcgc
    T S K F P S P L V V Y A N I R
1846 caaggagcctccccaattctcagggccagtggtcacagccctgatt
    Q G A S P I L R A S V T A L I
1891 gaatcagtgaatggaaaaacagttaccttggaaactactggataat
    E S V N G K T V T L E L L D N
1936 ggagcaggtgctgatgctactaaggatgacgggtgtctactcaagg
    G A G A D A T K D D G V Y S R
1981 tatttcacaacttatgacacgaatggtagatacagtgtaaaagt
    Y F T T Y D T N G R Y S V K V
2026 cgggctctgggaggagttaacgcagccagacggagagtgataccc
    R A L G G V N A A R R R V I P
2071 cagcagagtggagcactgtacatacctggctggattgagaatgat
    Q Q S G A L Y I P G W I E N D
2116 gaaatccaatggaatccaccaagacctgaaattaataaggatgat
    E I Q W N P P R P E I N K D D
2161 gttcaacacaagcaagtgtgtttcagcagaacatcctcgggaggg
    V Q H K Q V C F S R T S S G G
2206 tcatttgtggcttctgatgtcccaaagtctcccatacctgatctc
    S F V A S D V P N A P I P D L
2251 ttcccacctggccaaatcaccgacctgaaggcggaattcacggg
    F P P G Q I T D L K A E I H G
2296 ggcagtctcattaatctgacttggacagctcctggggatgattat
    G S L I N L T W T A P G D D Y
2341 gaccatggaacagctcacaaagtatatcattcgaataagtacaagt
    D H G T A H K Y I I R I S T S

```

**FIG. 4B3**

```
2386 attcttgatctcagagacaagttcaatgaatctcttcaagtgaat
      I L D L R D K F N E S L Q V N
2431 actactgctctcatcccaaaggaagccaactctgaggaagtcttt
      T T A L I P K E A N S E E V F
2476 ttgttttaaacagaaaacattacttttgaaaatggcacagatctt
      L F K P E N I T F E N G T D L
2521 ttcattgctattcaggctgttgataaggctgatctgaaatcagaa
      F I A I Q A V D K V D L K S E
2566 atatccaacattgcacgagtatctttgtttattcctccacagact
      I S N I A R V S L F I P P Q T
2611 ccgccagagacacctagtcctgatgaaacgtctgctccttgctcct
      P P E T P S P D E T S A P C P
2656 aatattcatatcaacagcaccattcctggcattcacatttttaaaa
      N I H I N S T I P G I H I L K
2701 attatgtggaagtggataggagaactgcagctgtcaatagcctag 2745
      I M W K W I G E L Q L S I A *
```

## FIG. 5A

CLUSTAL W (1.82) multiple sequence alignment of mouse and human ICACC proteins

```

mICACC-1: --MESLKSPVFLILHLLEGVLSESL-----IQLNNNGYEGIVIAIDHDVPEDEALIQH 52
hICACC-1  --MGPFKSSVFILILHLLEGALSNSL-----IQLNNNGYEGIVVAIDPNVPEDETLIQQ 52
hICACC-2: MTQRSIAGPICNLKFVTLVALSSELPLFLGAGVQLQDNGYNGLLIAINPQVPENQNLISN 60

mICACC-1: IKDMVTQASPYLFEATGKRFYFKNVAILIPESWKAKPEYTRPKLETFTKNADVLVSTTSPL 112
hICACC-1: IKDMVTQASLYLFEATGKRFYFKNVAILIPETWKTADYVRPKLETYKNADVLVAESTPP 112
hICACC-2: IKEMITEASFYLFNATKRRVFFRNIKILIPATWKAN-NNSKIKQESYEKANVIVTDWYRA 119

mICACC-1: GNDEPYTEHIGACGEKGIRIHLTPDFLAGKKLTQ-YGPQDRTFVHEWAHFRWGVFNEYNN 171
hICACC-1: GNDEPYTEQMGNCGEKGGERIHLTPDFIAGKKLAE-YGPQGRAFVHEWAHLRWGVFDEYNN 171
hICACC-2: HGDDPYTLQYRGCCKEGKYIHFTPNFLLNDNLTAGYGSRRGRVFVHEWAHLRWGVFDEYNN 179

mICACC-1: DEKFYLS-KGKPQAVRCSAAITGKNQVRRCCGGSCITNGKCVIDRVTGLYKDNCVFPDP 230
hICACC-1: DEKFYLS-NGRIQAVRCSAGITGTNVVKKCCGGSCYTK-RCTFNKXTGLYEKGCEFLVQS 229
hICACC-2: DKPFYINGQNQIKVTRCSSDITG---IFVCEKGPCEPQE-NCIISK---LFKEGCTFIYNS 232

mICACC-1: HQNEKASIMFNQNINSVVEFCTEKNHNQEAENDQNQRCLNRSTWEVIEQESDFKQTTPM- 289
hICACC-1: RQTEKASIMFAQHVDSEIVEFCTEQNHNKEAPNKQNKQCNLRSTWEVIRDSDFKKTTPM- 288
hICACC-2: TQSATASIMFMRLSSVVEFCNASTHNQEAENLQNMCSLRSALWDVITDSADFHHSFPMN 292

mICACC-1: -TAQPPAPTFSLLQIGQRIVCLVLDKSGSMLNDDRNLNRMNQASRLFLLQTVEQGSWVGMV 348
hICACC-1: -TTQPPNPFTFSLLQIGQRIVCLVLDKSGSMATGNRLNRLNQAGQLFLLQTVELGSWVGMV 347
hICACC-2: GTELPPPPTFSLVEAGDKVCLVLDASSKMAEADRLQLQQAEEFYLMQIVEIHTFVGIA 352

mICACC-1: TFDSAAYVQSELKQLNSGADRDLLIKHLPTVSAGGT--SICSGLRTAFTVIKKKY-PTDG 405
hICACC-1: TFDSAHHVQSELIQINSGSDRDTLAKRLPAAASGGT--SICSGLRSAFTVIRKKY-PTDG 404
hICACC-2: SFDSKGEIRAQLHQINSNDDRKLLVSYLPTTVSAKTDISICSGLKKGFVVEKLNKGKAYG 412

mICACC-1: SEIVLLTDGEDNTISSCFDLVKQSGAIIHTVALGPAAAKELEQLSKMTGGLQTYSSDQVQ 465
hICACC-1: SEIVLLTDGEDNTISGCFNEVKQSGAIIHTVALGPSAAQEELELSKMTGGLQTYASDQVQ 464
hICACC-2: SVMILVTSGDDKLLGNCLPTVLSSGSTIHSIALGSSAAPNLEELSRLTGGLKFFVDPDISN 472

mICACC-1: NNGLVDFAALSSGNAAIAQHSIQLESRGVNLQNNQWMNGSVIVDSSVGKDTLFLITWTT 525
hICACC-1: NNGLIDAFGALSSGNAAVQSRSIQLESKGLTLQNSQWMNGTVIVDSTVGKDTLFLITWTT 524
hICACC-2: SNSMIDAFSRISSTGDIQQHIQLESTGENVKPHHQLKNTVTVDNVTGNDTMFLVTWQA 532

mICACC-1: H-PPTIFIWDPSGVE--QNGFILDTTTKVAYLQVPGTAKVGFWKYSIQ---ASSQTLTLT 579
hICACC-1: Q-PPQILLWDPSGQK--QGGFVVDKNTKMAYLQIPGIAKVGTWKYSLQ---ASSQTLTLT 578
hICACC-2: SGPPEIILFDPDGRKYTYNNFITNLTFRTASLWIPGTAKPGHWYTLNNTTHSLQALKVT 592

```

## FIG. 5B

mICACC-1: VTSRAASATLPPITVTPVVNKNKGKFPSPVTVYASIRQGASPILRASVTALIESVNGKTV 639  
hICACC-1: VTSRASNATLPPITVTSKTNKDTSKFPSPLVVYANIRQGASPILRASVTALIESVNGKTV 638  
hICACC-2: VTSRASNSAVPPATVEAFVERDSLHFPHPVMIYANVKQGFYPILNATVTATVEPETGDPV 652

mICACC-1: TLELLDNGAGADATKNDGVYSRFFTAFDANGRYSVKIWALGGVTSRQRAAPPKNRAMYI 699  
hICACC-1: TLELLDNGAGADATKDDGVYSRYFTTYDTNGRYSVKVRALGGVNAARRRVIPQQSGALYI 698  
hICACC-2: TLRLDDGAGADVIKNDGIYSRYFFSFAANGRYSLKVHVNHSPSISTPAHSIPGSHAMYV 712

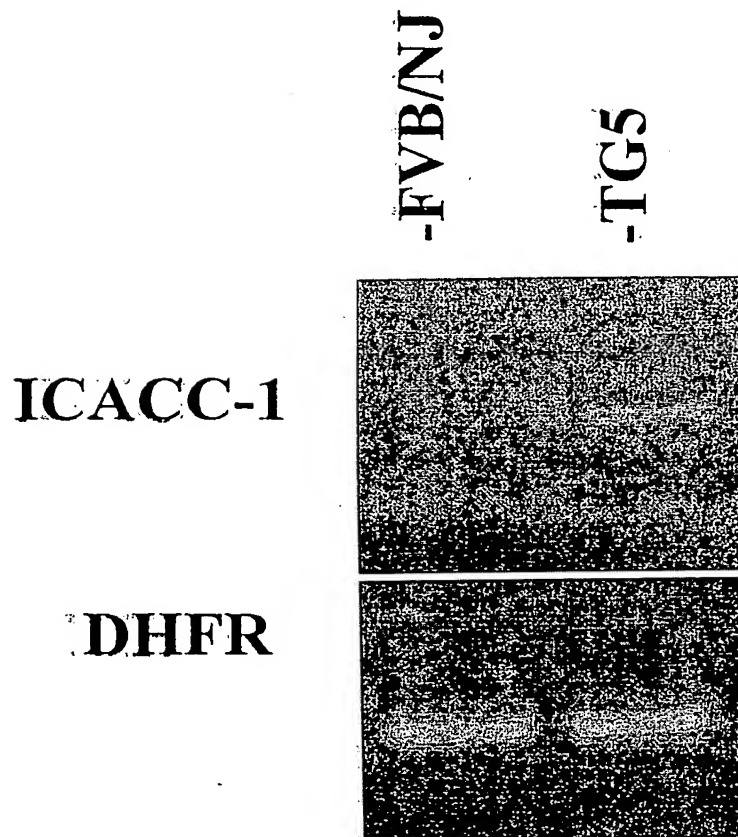
mICACC-1: DGWIEDGEVRMNPFRPETS--YVQDKQLCFSTRSSGGSFVATNPVAAAPIPDLFPFPCQIT 757  
hICACC-1: PGWIENDEIQWNPPRPEINKDDVQHKQVCFSRTSSGGSFVASDVPN-APIPDLFPFPGQIT 757  
hICACC-2: PGYTANGNIQMNA PRKSVGR-NEEERKWGFSRVSSGGSFVSLGVPA-GPHPDVFPFCKII 770

mICACC-1: DLKASIQQQLVNLWTWAPGDDYDHGRASNYIIRMSTSIVDLRDHFNTSLQVNTTGLIPK 817  
hICACC-1: DLKAEIHGGSLINLTWAPGDDYDHGTAHKYIIRISTSIILDLRDKFNESLQVNTTALIPK 817  
hICACC-2: DLEAVKVEEBELT-LSWTAPGEDFDQQGATS YEIRMSKSLQNIQDDFNAILVNTSKRNPQ 829

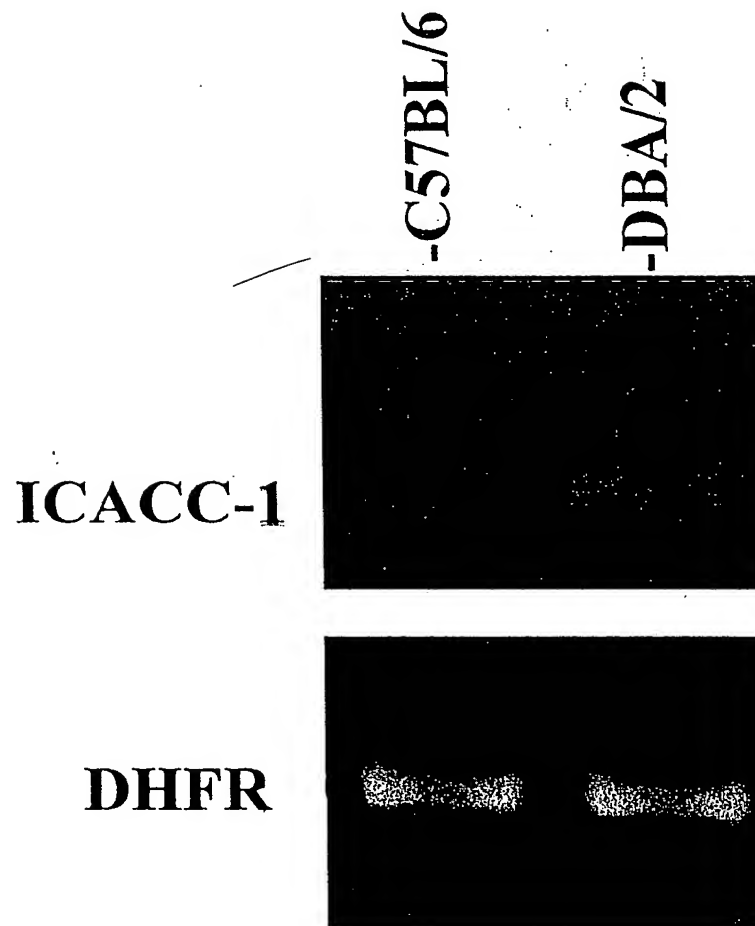
mICACC-1: EASSEEIFEFELGGNTFG-----NG-----TDIFIAIQAVDKSNLKSEISNIARVS VFIP 867  
hICACC-1: EANSEEVFLFKPENITFE-----NG-----TDLFIAIQAVDKVDLKSEISNIARVSLFIP 867  
hICACC-2: QAGIREIFTFSPQISTNGPEHQPNGETHESHRIYVAIRAMD RNSLQSAVS NIAQAPLFIP 889

mICACC-1: AQEP---PIPEDSTPPCPDISINSTIPGIHVLKIMWKWLGEMQVTLGLH----- 913  
hICACC-1: PQTPPETPSPDETSAPCPNIHINSTIPGIHILKIMWKWIGELQLSIA----- 914  
hICACC-2: PNSD---PVPARDYLILKGVL TAMGLIGIICLIIVVTHHTLSRKKRADKKENGTKLL 943

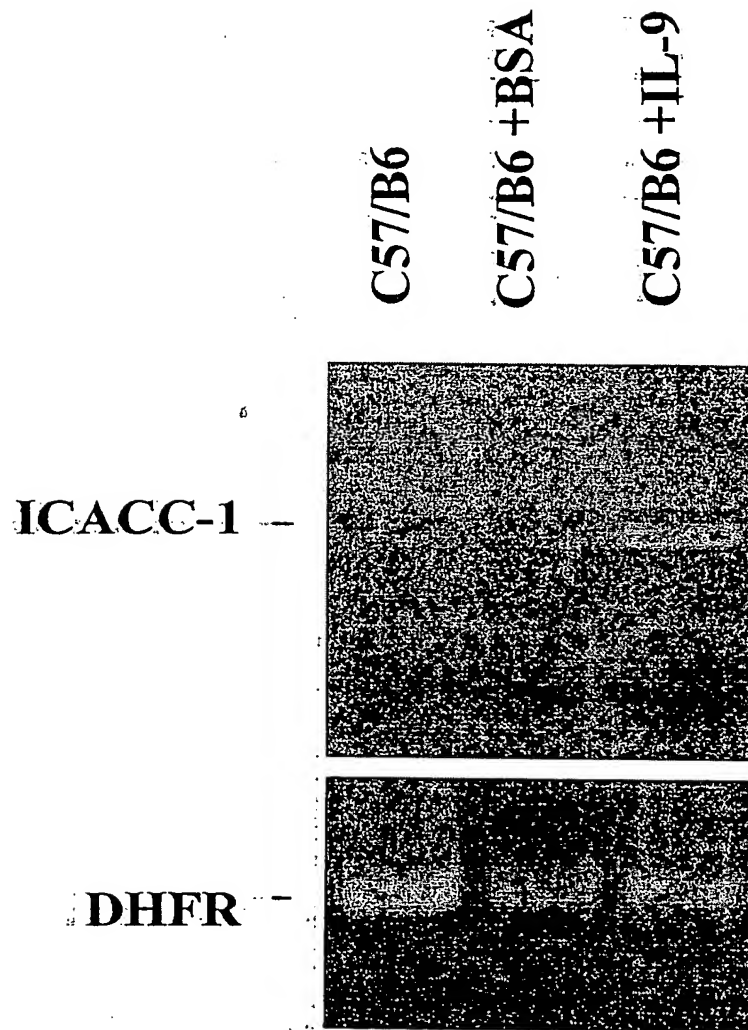
**FIG. 6**



**FIG. 7**



**FIG. 8**



# IL-9 Transgenic Mouse

1. uterus
2. thymus
3. testis
4. stomach
5. Spleen
6. sml. intestine
7. ovary
8. muscle
9. lymph nodes
10. lung
11. liver
12. kidney
13. heart
14. colon
15. brain



FIG. 9A

# Normal Mouse

1. heart
2. brain
3. spleen
4. lung
5. liver
6. skeletal muscle
7. kidney
8. testis

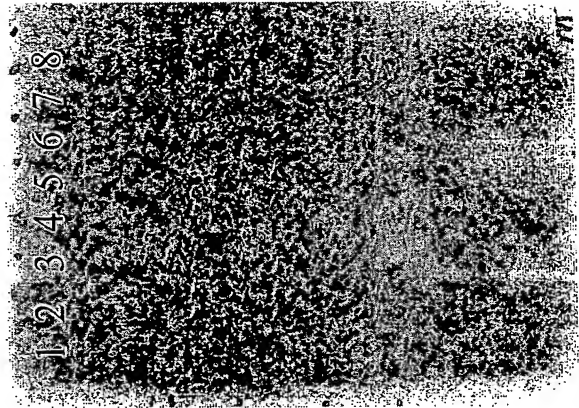
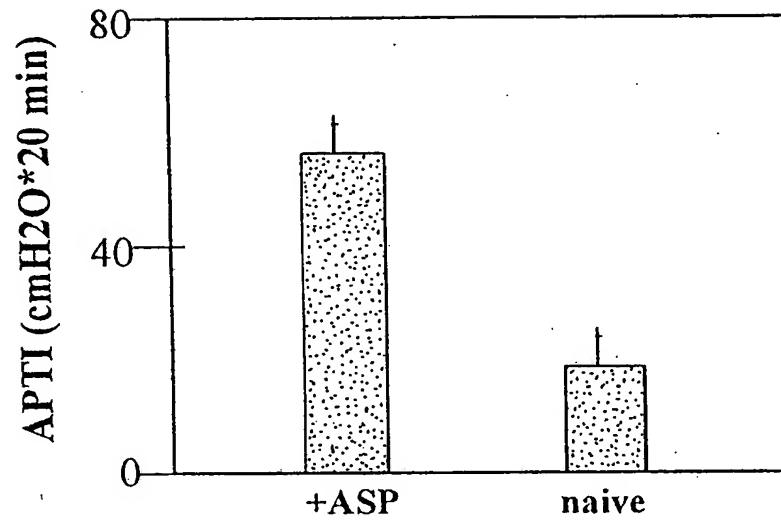
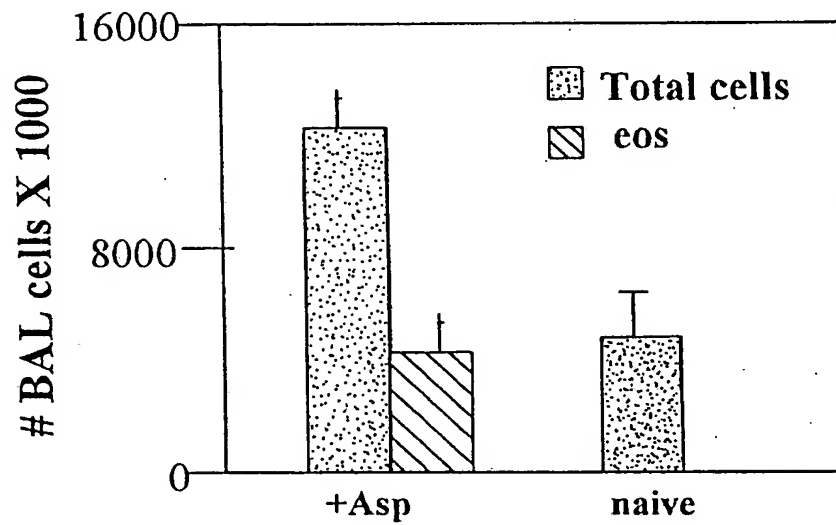


FIG. 9B

**FIG. 10A**

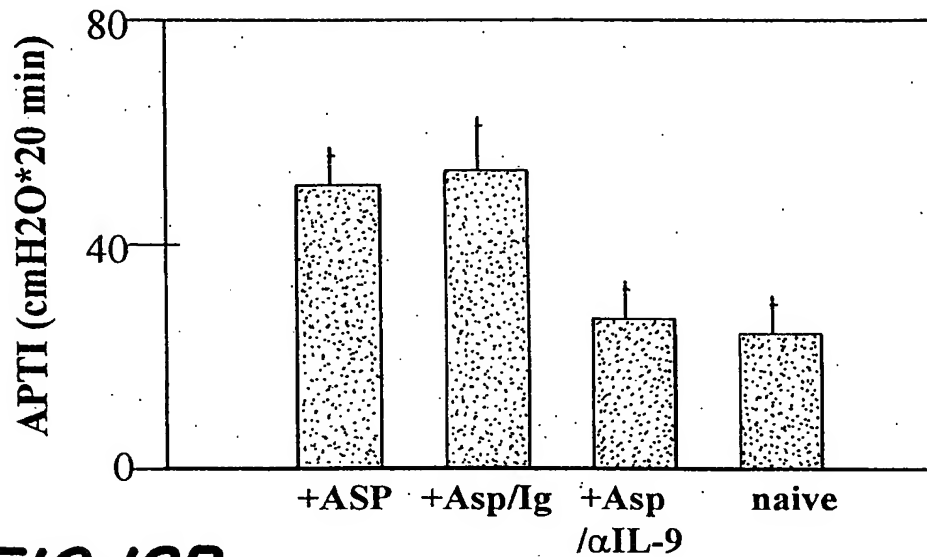


**FIG. 10B**

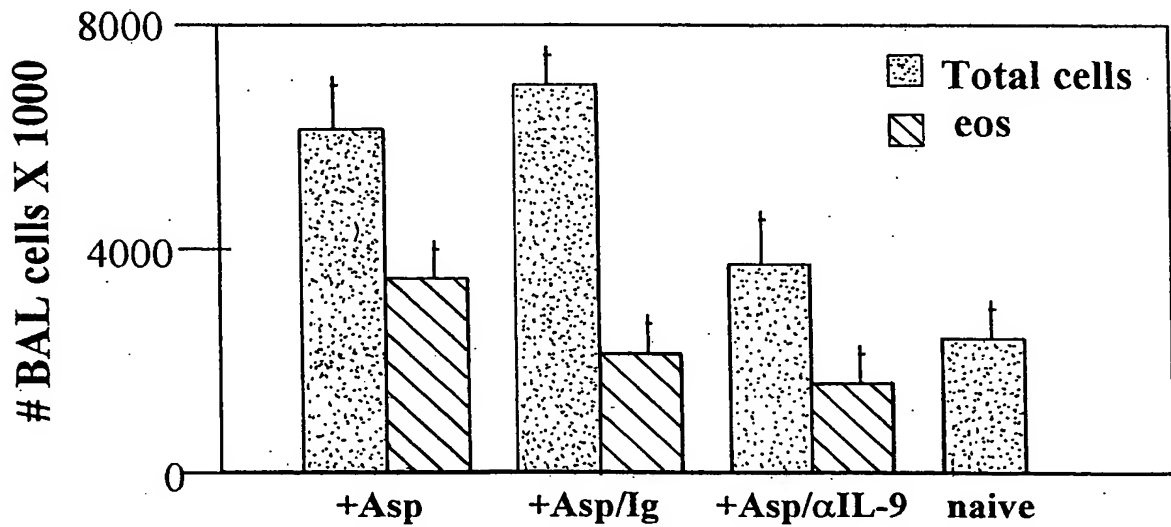




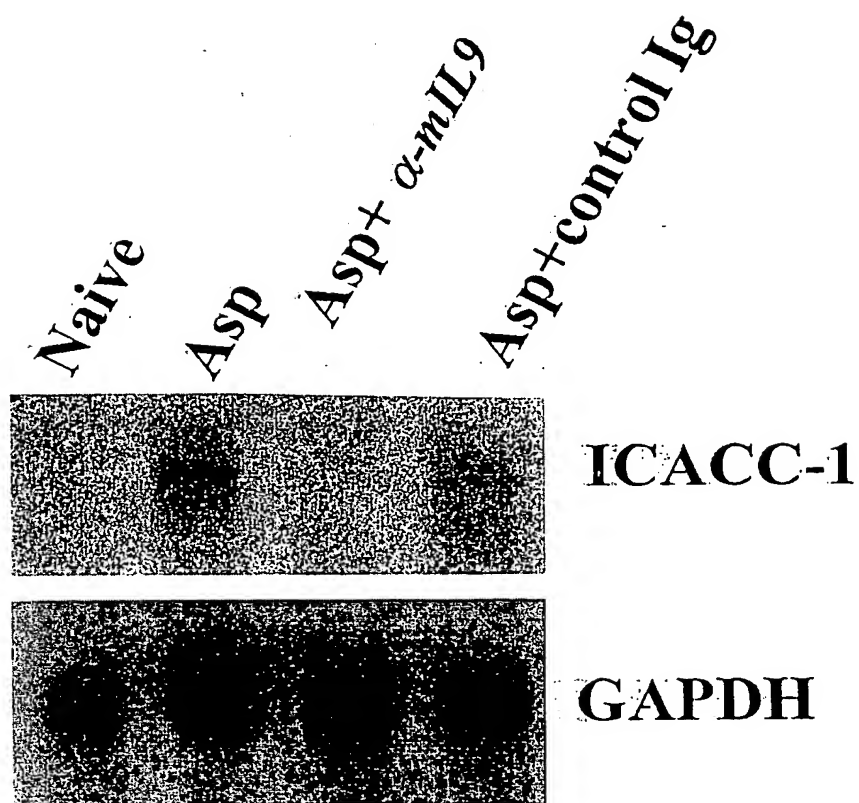
**FIG. 12A**



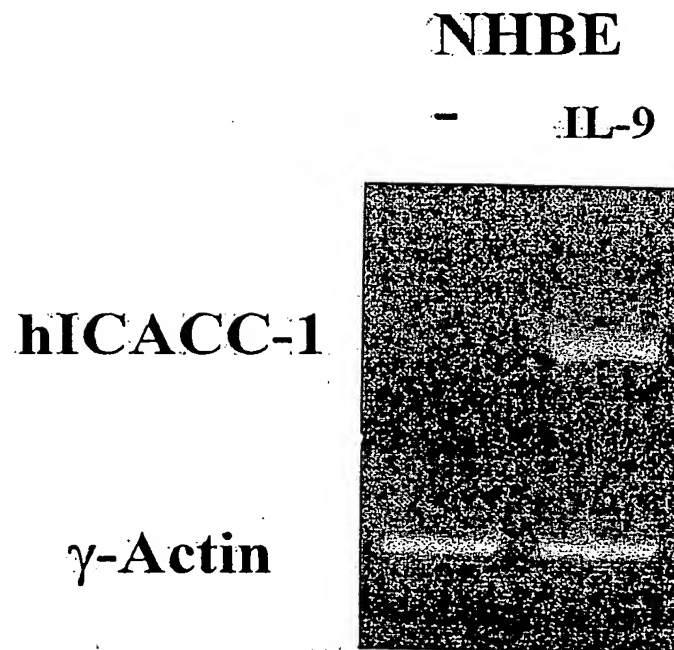
**FIG. 12B**



**FIG. 13**



**FIG. 14**

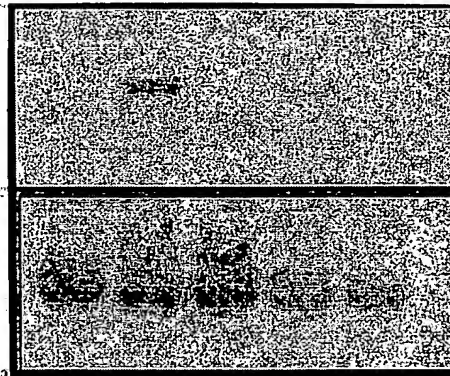


# FIG. 15

Patient

1 2

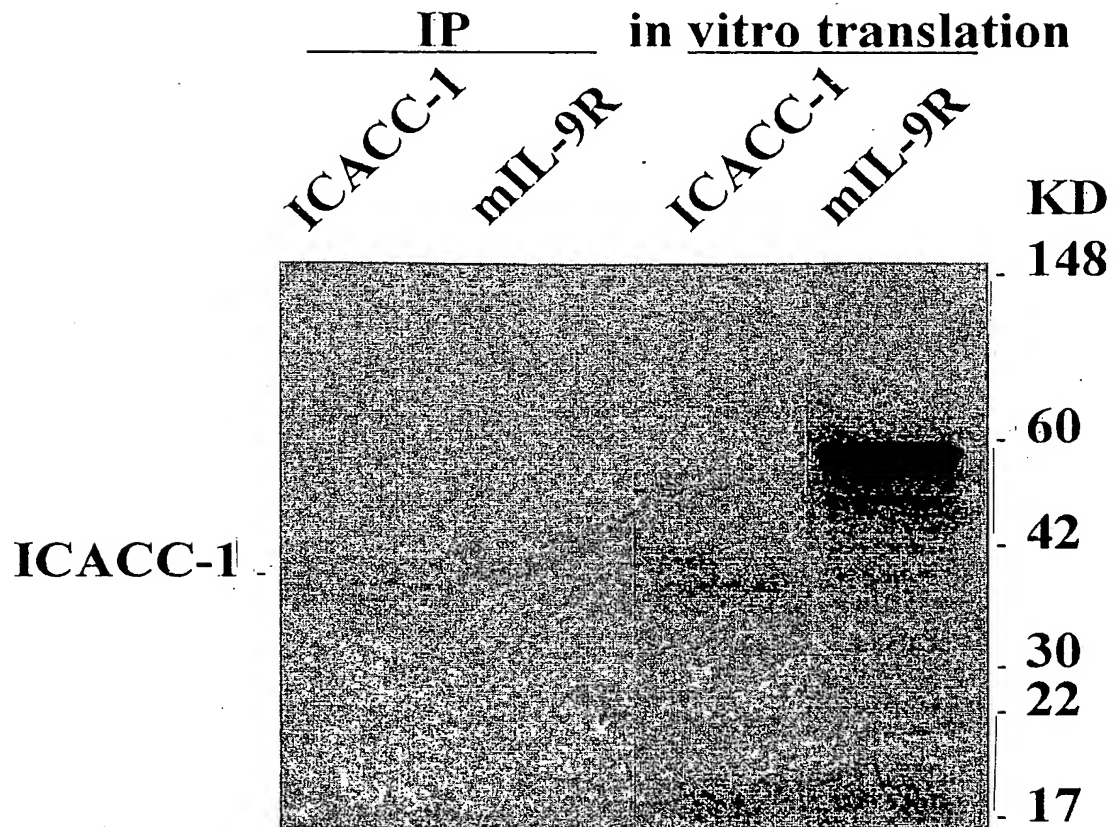
hIL-9 - + - + c



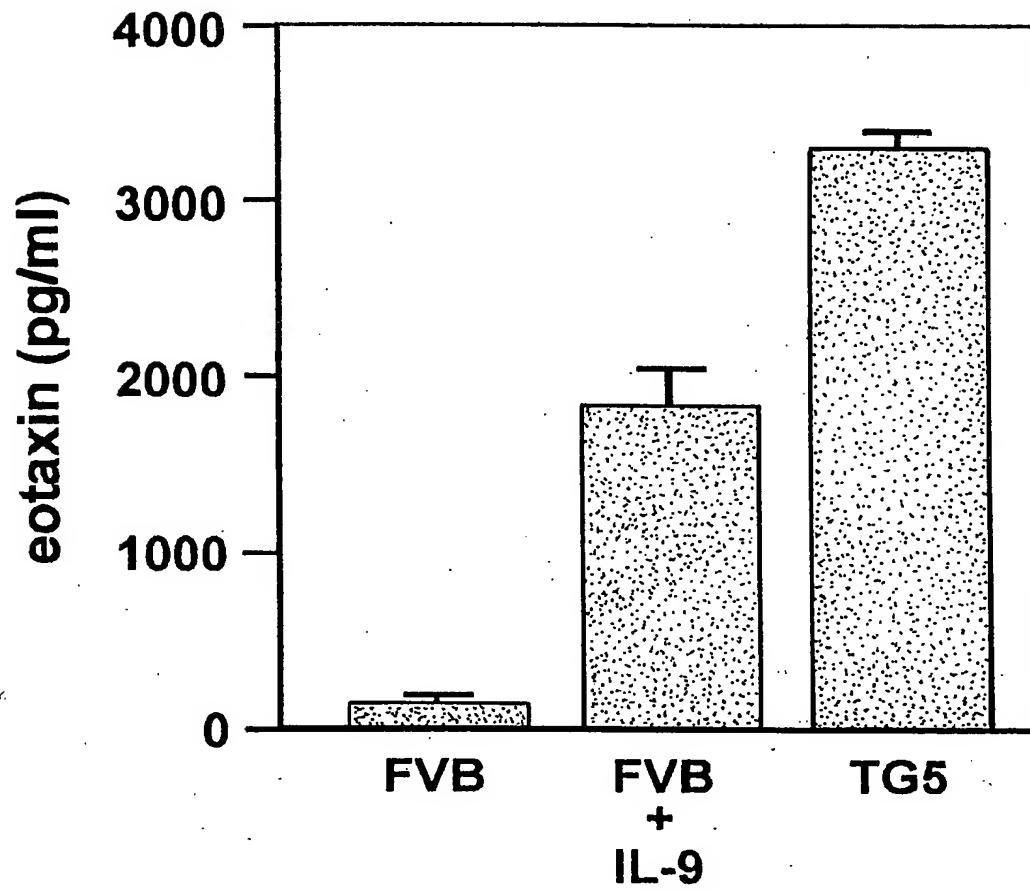
hICACC-1

hPMS2

**FIG. 16**



**FIG. 17**



**FIG. 18**

